```
   1 TCCGCCCCCG GCCCGGGGTG CGAATCCGGT GCCGGCAAGC GGCTGGCGAT
  51 GCTGGAGGTT CGCTAGCCGA AGCGGCTGCA TCTGGCGCCG CGTCTGCCCC
 101 GCGTGCTCGG AGCGGATTCT GCCCGCCGTC CCCGGAGCCC TCGGCGCCCC
 151 GCTGAGCCCG CGATCACTTC CTCCCTGTGA CCAACCGGCG CTGCAGGTTA
 201 GAGCCTGGCA ATGCCGTTTG GGTGTGTGAC TCTGGGCGAC AAGAAGAACT
 251 ATAACCAGCC ATCGGAGGTG ACTGACAGAT ATGATTTGGG ACAGGTCATC
 301 AAGACTGAGG AGTTTTGTGA AATCTTCCGG GCCAAGGACA AGACGACAGG
 351 CAAGCTGCAC ACCTGCAAGA AGTTCCAGAA GCGGGACGGC CGCAAGGTGC
 401 GGAAAGCTGC CAAGAACGAG ATAGGCATCC TCAAGATGGT GAAGCATCCC
 451 AACATCCTAC AGCTGGTGGA TGTGTTTGTG ACCCGCAAGG AGTACTTTAT
 501 CTTCCTGGAG CTGGCCACGG GGAGGGAGGT GTTTGACTGG ATCCTGGACC
 551 AGGGCTACTA CTCGGAGCGA GACACAAGCA ACGTGGTACG GCAAGTCCTG
 601 GAGGCCGTGG CCTATTTGCA CTCACTCAAG ATCGTGCACA GGAATCTCAA
 651 GCTGGAGAAC CTGGTTTACT ACAACCGGCT GAAGAACTCG AAGATTGTCA
 701 TCAGTGACTT CCATCTGGCT AAGCTAGAAA ATGGCCTCAT CAAGGAGCCC
 751 TGTGGGACCC CCGAGTATCT GGCCCCAGAG GTGGTAGGCC GGCAGCGGTA
 801 TGGACGCCCT GTGGACTGCT GGGCCATTGG AGTCATCATG TACATCCTGC
 851 TTTCAGGCAA TCCACCTTTC TATGAGGAGG TGGAAGAAGA TGATTATGAG
 901 AACCATGATA AGAATCTCTT CCGCAAGATC CTGGCTGGTG ACTATGAGTT
 951 TGACTCTCCA TATTGGGATG ATATTTCGCA GGCAGCCAAA GACCTGGTCA
1001 CAAGGCTGAT GGAGGTGGAG CAAGACCAGC GGATCACTGC AGAAGAGGCC
1051 ATCTCCCATG AGTGGATTTC TGGCAATGCT GCTTCTGATA AGAACATCAA
1101 GGATGGTGTC TGTGCCCAGA TTGAAAAGAA CTTTGCCAGG GCCAAGTGGA
1151 AGAAGGCTGT CCGAGTGACC ACCCTCATGA AACGGCTCCG GGCACCAGAG
1201 CAGTCCAGCA CGGCTGCAGC CCAGTCGGCC TCAGCCACAG ACACTGCCAC
1251 CCCCGGGGCT GCAGGTGGGG CCACAGCTGC AGCTGCGAGT GGAGCTACCT
1301 CAGCCCCTGA GGGTGATGCT GCTCGTGCTG CAAAGAGTGA TAATGTGGCC
1351 CCCGCAGACC GTAGTGCCAC CCCAGCCACA GATGGAAGTG CCACCCCAGC
1401 CACTGATGGC AGTGTCACCC CAGCCACCGA TGGAAGCATC ACTCCAGCCA
1451 CTGATGGGAG TGTCACCCCA GTCACTGACA GGAGCGCTAC TCCAGCCACT
1501 GATGGGAGAG CCACACCAGC CACAGAAGAG AGCACTGTGC CCACCACCCA
1551 AAGCAGTGCC ATGCTGGCCA CCAAGGCAGC TGCCACCCCT GAGCCGGCTA
1601 TGGCCCAGCC GGACAGCACA GCCCCAGAGG GCGCCACAGG CCAGGCTCCA
1651 CCCTCTAGTA AAGGGGAAGA GGCTGCTGGT TATGCCCAGG AGTCTCAAAG
1701 GGAGGAGGCC AGCTGAGTAG GCAGCCTGGT GAGGGGGGGC AGGGGATGGG
1751 CAGGAGGGTG GGAGAGTGGA TGAGGGGCTT CTCACTGTAC ATAGAGTCAC
1801 TGGCATGATG CCCTCGCTCC CCCATGCCCC CACATCCCAG TGGGGCATAA
1851 CTAGGGGTCA CGGGAGAGCA GTCTCGTCTC CTGTGTGTAT GTGTGTGAGT
1901 GGTGGGCAGG CCAGTGGCAG GGCCGGCCCC AGCCCCTGCA TGGATTCCTT
1951 GTGGCTTTTC TGTCTTTTGC TAGCTTCACC AGTTTCTGTT CCTTGTGGGA
2001 TGCTGCTCTA GGGATACTCA GGGGGCTCCT GCTCTCCTTC CCCTTCCCTT
2051 CTTGCCTCAC CATTCCCCTA GGCAGGCCCT GCAGGTCCCA CACTCTCCCA
2101 GGCCCTAAAC TTGGGCGGCC TTGCCCTGAG AGCTGGTCCT CCAGCGAGGC
2151 CCTGTCAGCG GTCTTAGGCT CCTGCACATG AAGGTGTGTG CCTGTGGTGT
2201 GTGGGCTGCT CTAGGAGCAG ATACAGGCTG GTATAGAGGA TGCAGAAAGG
2251 TAGGGCAGTA TGTTTAAGTC CAGACTTGGC ACATGGCTAG GGATACTGCT
2301 CACTAGCTGT GGAGGTCCTC AGGAGTGGAG AGAATGAGTA GGAGGGCAGA
2351 AGCTTCCATT TTTGTCCTTC CTAAGACCCT GTTATTTGTG TTATTTCCTG
2401 CCTTTCCGAG TCCTGCAGTG GGCTGCCCTG TACCCTGAAC CTCATGAGCC
2451 TCTAAGGGAA AGGAGGAACA ATTAGGACGT GGCAATGAGA CCTGGCAGGG
2501 CAGAGTACAA GCCCAGCACC CAGTGTCCCA GCCTTACTGG GTCCTTACCC
2551 TGGGCCAAAC AGGGAGGGCT GATACCTCCT TGCTCTTCCT AGATGCCCAC
2601 CTCCTACAAT CTCAGCCCAC AAGTCCTCTC CACCCTAGGG GGCTTGCTGC
2651 ATGGCAATAA CTCATAATCT GATTTGGAGG TTTGCCCTTT ACAGGGGCAG
2701 ATTTTCTGCT CAGTTCAACA ATGAAATGAA GAGGAACTCC CTCTTTCTAC
2751 AGCTCACTTC TATCAGAGGC CCAGGTGCCT CAGAGCCACA TTGAGTTGCT
2801 TTTTCTGGGA TGAGGAAGTA GGGTTAAACT CCCCAGTTTC CTGAGGGAGG
2851 CTCCTGACAG GTGCCCTTTG TCAGACCCTA CCACAGCCTG GATAGGCAGC
2901 CACATTGGTC CTCGCCCTTG CTCGGCACTC CGTGGTGGTC CTGCCCTTCT
```

FIGURE 1A

```
2951 CCCTGCATGC CTGTGGGTCT GCTCTGGTGT GTGAAGGTCG GTGGGTTAAC
3001 TGTGTGCCTA CTGAACCTGG CAAATAAACA TCACCCTGCA AAGCCAAAAA
3051 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3101 AAAAAAAAAA AAAAAAAAAA AAAA
```

FEATURES:
5'UTR: 1 - 210
Start Codon: 211
Stop Codon: 1714
3'UTR: 1717

Homologous proteins:
Top 10 BLAST Hits

	Score	E
gi|2143639|pir||I56542 calmodulin-binding protein - rat >gi|349...	929	0.0
gi|7521914|pir||T30814 calmodulin-binding protein kinase - Fugu...	598	e-170
gi|3122310|sp|Q63450|KCC1_RAT CALCIUM/CALMODULIN-DEPENDENT PROT...	310	4e-83
gi|4502553|ref|NP_003647.1| calcium/calmodulin-dependent protei...	309	9e-83
gi|3114436|pdb|1A06| Calmodulin-Dependent Protein Kinase Fro...	303	7e-81
gi|406113|gb|AAA19670.1| (L24907) protein kinase I [Rattus norv...	299	1e-79
gi|9966875|ref|NP_065130.1| CamKI-like protein kinase [Homo sap...	299	1e-79
gi|3893099|emb|CAA76937.1| (Y17917) calcium/calmodulin dependen...	288	3e-76
gi|4007153|emb|CAA19296.1| (AL023754) dJ272L16.1 (Rat Ca2+/Calm...	286	1e-75
gi|4678722|emb|CAB41259.1| (AL049688) hypothetical protein [Hom...	286	1e-75

BLAST to dbEST:

	Score	E
gi|11264319 /dataset=dbest /taxon=96...	1057	0.0
gi|11126214 /dataset=dbest /taxon=96...	989	0.0
gi|11259094 /dataset=dbest /taxon=96...	963	0.0
gi|11260705 /dataset=dbest /taxon=96...	896	0.0
gi|708663 /dataset=dbest /taxon=9606 /...	611	e-172
gi|10215012 /dataset=dbest /taxon=96...	601	e-169
gi|11099650 /dataset=dbest /taxon=960...	577	e-162
gi|831534 /dataset=dbest /taxon=9606 /...	535	e-150
gi|9136656 /dataset=dbest /taxon=9606...	529	e-148
gi|2001736 /dataset=dbest /taxon=9606 ...	509	e-142

EXPRESSION INFORMATION FOR MODULATORY USE:
library source:
Expression information from BLAST dbEST hits:
gi|11264319 Brain
gi|11126214 Lung
gi|11259094 Brain
gi|11260705 Brain
gi|708663 Infant brain
gi|10215012 Lung
gi|11099650 Brain
gi|831534 Infant brain
gi|9136656 Brain
gi|2001736 Infant brain

Expression information from PCR-based tissue screening panels:
Infant brain, hippocampus

FIGURE 1B

```
  1 MPFGCVTLGD KKNYNQPSEV TDRYDLGQVI KTEEFCEIFR AKDKTTGKLH
 51 TCKKFQKRDG RKVRKAAKNE IGILKMVKHP NILQLVDVFV TRKEYFIFLE
101 LATGREVFDW ILDQGYYSER DTSNVVRQVL EAVAYLHSLK IVHRNLKLEN
151 LVYYNRLKNS KIVISDFHLA KLENGLIKEP CGTPEYLAPE VVGRQRYGRP
201 VDCWAIGVIM YILLSGNPPF YEEVEEDDYE NHDKNLFRKI LAGDYEFDSP
251 YWDDISQAAK DLVTRLMEVE QDQRITAEEA ISHEWISGNA ASDKNIKDGV
301 CAQIEKNFAR AKWKKAVRVT TLMKRLRAPE QSSTAAAQSA SATDTATPGA
351 AGGATAAAAS GATSAPEGDA ARAAKSDNVA PADRSATPAT DGSATPATDG
401 SVTPATDGSI TPATDGSVTP VTDRSATPAT DGRATPATEE STVPTTQSSA
451 MLATKAAATP EPAMAQPDST APEGATGQAP PSSKGEEAAG YAQESQREEA
501 S
```

FEATURES:
Functional domains and key regions:
[1] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 11

1	21-23	TDR
2	422-424	TDR
3	46-48	TGK
4	51-53	TCK
5	91-93	TRK
6	103-105	TGR
7	118-120	SER
8	138-140	SLK
9	292-294	SDK
10	21-23	TDR
11	422-424	TDR

[2] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 10

1	7-10	TLGD
2	91-94	TRKE
3	103-106	TGRE
4	118-121	SERD
5	276-279	TAEE
6	341-344	SATD
7	364-367	SAPE
8	470-473	TAPE
9	483-486	SKGE
10	495-498	SQRE

[3] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 2

1	127-135	RQVLEAVAY
2	484-491	KGEEAAGY

FIGURE 2A

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 4
1 288-293 GNAASD
2 349-354 GAAGGA
3 352-357 GGATAA
4 353-358 GATAAA

[5] PDOC00009 PS00009 AMIDATION
Amidation site

59-62 DGRK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	207	227	1.342	Certain
2	351	371	1.250	Certain

BLAST Alignment to Top Hit:
>gi|2143639|pir||I56542 calmodulin-binding protein - rat
gb|AAA16633.1| (L22557) calmodulin-binding protein [Rattus norvegicus]
Length = 504

Score = 929 bits (2375), Expect = 0.0
Identities = 468/509 (91%), Positives = 473/509 (91%), Gaps = 8/509 (1%)
Frame = +1

```
Query: 211  MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 390
            MPFGCVTLGDKKNYNQPSEVTDRYDLGQV+KTEEFCEIFRAKDKTTGKLHTCKKFQKRDG
Sbjct: 1    MPFGCVTLGDKKNYNQPSEVTDRYDLGQVVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 60

Query: 391  RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
            RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61   RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 750
            DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP
Sbjct: 121  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 180

Query: 751  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
            CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI
Sbjct: 181  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 240

Query: 931  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 1110
            LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV
Sbjct: 241  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 300

Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAAQSASATDTATPGAAGGATAAAAS 1290
            CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQS TAA      +D ATPGAAGGA AAAA
Sbjct: 301  CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSGTAA-----TSDAATPGAAGGAVAAAAG 355

Query: 1291 G--------ATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITP 1446
            G        AT    GDA  AAKSD++A ADRSATPATDGSATPATDGSVTPATDGSITP
Sbjct: 356  GAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVTPATDGSITP 415
```

FIGURE 2B

```
Query: 1447 ATDGSVTPVTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAP 1626
            ATDGSVTP TDRSATPATDGRATPATEESTVP  QSSA  A KAAATPEPA+AQPDSTA
Sbjct: 416  ATDGSVTPATDRSATPATDGRATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTAL 475

Query: 1627 EGATGQAPPSSKGEEAAGYAQESQREEAS 1713
            EGATGQAPPSSKGEEA G AQESQR E S
Sbjct: 476  EGATGQAPPSSKGEEATGCAQESQRVETS 504


 Score = 34.4 bits (77), Expect = 7.1
 Identities = 42/158 (26%), Positives = 60/158 (37%), Gaps = 5/158 (3%)
 Frame = -3

Query: 1673 ASSPLLEGGAWPVAPSGAVLSGWAIA--GSGVAAALVASMALLWVVGTVLSSVAGVALPS 1500
            A++P   GGA   A  GA  +  A A  G+G  A   A            ++S    A P+
Sbjct: 340  AATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAK-------SDDMASADRSATPA 392

Query: 1499 VAGVALLSVTGVTLPSVAGVMLPSVAGVTLPSVAGVALPSVAGVALRSAGATLSLFAARA 1320
               G A  +  G   P+  G + P+  G   P+    A P+  G
Sbjct: 393  TDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDG----------------R 436

Query: 1319 ASPSGAEVAPLAAAAVAPPAAPGVAV---SVAEADWAA 1215
            A+P+  E    AA + A PAA   A    +VA+ D  A
Sbjct: 437  ATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTA 474


>gi|7521914|pir||T30814 calmodulin-binding protein kinase - Fugu
          rubripes
 emb|CAA09101.1| (AJ010348) calmodulin binding protein kinase [Fugu rubripes]
         Length = 421

 Score =  598 bits (1526), Expect = e-170
 Identities = 296/391 (75%), Positives = 332/391 (84%), Gaps = 2/391 (0%)
 Frame = +1

Query: 211  MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 390
            MPFGC+TLG+KK+YN PSEVTD+YDLGQV+K+EEFCEIFRAKD+ T K++TCKKF K+DG
Sbjct: 1    MPFGCLTLGEKKDYNSPSEVTDKYDLGQVVKSEEFCEIFRAKDRNTLKMYTCKKFNKKDG 60

Query: 391  RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
            RKVRKAAKNEI ILKMVKH NILQLVD F T+KEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61   RKVRKAAKNEIMILKMVKHHNILQLVDAFETKKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 750
            DTSNV+RQVLEAVAYLHSLKIVHRNLK  NLVY+NRLK+SKIVISDF LAKLENGLIK+P
Sbjct: 121  DTSNVMRQVLEAVAYLHSLKIVHRNLK--NLVYFNRLKHSKIVISDFQLAKLENGLIKDP 178

Query: 751  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
            CGTPEYLAPEV+GRQRYGRPVDCWAIGVIMYILLSGNPPFY++ +E+D ++ DKNLF KI
Sbjct: 179  CGTPEYLAPEVIGRQRYGRPVDCWAIGVIMYILLSGNPPFYDDGDEEDSDSRDKNLFLKI 238

Query: 931  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 1110
            L+GDYEFDSPYWDDIS +AK LV  LMEV+QDQR+TA+EAI+HEWISGNAASDKNIKDGV
Sbjct: 239  LSGDYEFDSPYWDDISDSAKTLVASLMEVDQDQRLTAQEAIAHEWISGNAASDKNIKDGV 298
```

FIGURE 2C

```
Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAAQSASAT--DTATPGAAGGATAAA 1284
            CAQIEKNFA+AKWKKAVRVTTLMKRLRA EQ  T A+  A+         P   GG+  AA
Sbjct: 299  CAQIEKNFAKAKWKKAVRVTTLMKRLRASEQGDTGASGLAAGATGGPPDPNMPGGSLLAA 358

Query: 1285 ASGATSAPEGDAARAAKSDNVAPADRSATPA 1377
                       + + A S+  A A  S  P+
Sbjct: 359  ----------SIKTALSEKAADAQTSTIPS 378


>gi|3122310|sp|Q63450|KCC1_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN
          KINASE TYPE I (CAM KINASE I)
 pir||S50193 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 gb|AAA66944.1| (L26288) CaM-like protein kinase [Rattus norvegicus]
 prf||2024225A Ca/calmodulin protein kinase I [Rattus norvegicus]
        Length = 374

 Score =  310 bits (787), Expect = 4e-83
 Identities = 156/357 (43%), Positives = 226/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+        + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +     ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E         +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLRAPE--QSSTAAAQSASATDTATPGAAGGATAAAASGATSAP 1308
            KWK+A   T +++ +R  +   S     Q+AS  + TP A G A           P
Sbjct: 302  KWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTPTAGGPAAGCCCRDCCVEP 358


 >gi|4502553|ref|NP_003647.1| calcium/calmodulin-dependent protein
           kinase I [Homo sapiens]
  sp|Q14012|KCC1_HUMAN CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (CAM KINASE I)
  pir||S57347 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
  gb|AAA99458.1| (L41816) cam kinase I [Homo sapiens]
         Length = 370

  Score =  309 bits (784), Expect = 9e-83
  Identities = 156/357 (43%), Positives = 225/357 (62%), Gaps = 4/357 (1%)
  Frame = +1
```

FIGURE 2D

```
Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K  K         + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +    ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLRAPE--QSSTAAAQSASATDTATPGAAGGATAAAASGATSAP 1308
            KWK+A   T +++ +R  +   S     Q+AS  + TP A G A            P
Sbjct: 302  KWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTPVAGGPAAGCCCRDCCVEP 358


>gi|3114436|pdb|1A06|    Calmodulin-Dependent Protein Kinase From Rat
          Length = 332

 Score =  303 bits (768), Expect = 7e-81
 Identities = 146/316 (46%), Positives = 213/316 (67%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K  K+         + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +    ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLR 1191
            KWK+A   T +++ +R
Sbjct: 302  KWKQAFNATAVVRHMR 317
```

FIGURE 2E

```
>gi|406113|gb|AAA19670.1| (L24907) protein kinase I [Rattus
          norvegicus]
         Length = 332

 Score =  299 bits (758), Expect = 1e-79
 Identities = 146/316 (46%), Positives = 212/316 (66%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+       + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +     ++ ++L +G E+FD I+++G Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGGYTERDRSRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E         +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLR 1191
            KWK+A   T +++ +R
Sbjct: 302  KWKQAFNRTAVVRHMR 317


>gi|9966875|ref|NP_065130.1| CamKI-like protein kinase [Homo sapiens]
 gb|AAG00534.1|AF286366_1 (AF286366) CamKI-like protein kinase [Homo sapiens]
         Length = 357

 Score =  299 bits (757), Expect = 1e-79
 Identities = 142/332 (42%), Positives = 221/332 (65%), Gaps = 2/332 (0%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q  ++   + + T  F E+  A++K TGKL   K   K+  +    + +NEI +L+
Sbjct: 15   QAEDIKKIFEFKETLGTGAFSEVVLAEEKATGKLFAVKCIPKKALKGKESSIENEIAVLR 74

Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
             +KH NI+ L D++ +     ++ ++L +G E+FD I+++G+Y+E+D S ++RQVL+AV Y
Sbjct: 75   KIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAVYY 134

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE--NGLIKEPCGTPEYLAPEVVG 789
            LH + IVHR+LK ENL+YY++ + SKI+ISDF L+K+E    ++  CGTP Y+APEV+
Sbjct: 135  LHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVLA 194

Query: 790  RQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWD 969
            ++ Y + VDCW+IGVI YILL G PPFY+E         +D  LF +IL  +YEFDSPYWD
Sbjct: 195  QKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDSKLFEQILKAEYEFDSPYWD 246
```

FIGURE 2F

```
Query: 970  DISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKW 1149
            DIS +AKD +  LME + ++R T E+A  H WI+G+ A +KNI + V AQI KNFA++KW
Sbjct: 247  DISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKW 306

Query: 1150 KKAVRVTTLMKRLRAPEQSSTAAAQSASATDT 1245
            ++A   T +++ +R      S+  + +AS + +
Sbjct: 307  RQAFNATAVVRHMRKLHLGSSLDSSNASVSSS 338


>gi|3893099|emb|CAA76937.1| (Y17917) calcium/calmodulin dependent
          protein kinase I [Drosophila melanogaster]
 gb|AAF59343.1| (AE003844) CaMKI gene product [alt 2] [Drosophila melanogaster]
          Length = 405

 Score =  288 bits (729), Expect = 3e-76
 Identities = 152/388 (39%), Positives = 243/388 (62%), Gaps = 21/388 (5%)
 Frame = +1

Query: 238  DKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTT-GKLHTCKKFQKRDGRKVRKAAK 414
            D K  N+   + ++Y+L  ++ T  F E+  A+ K + G+    K   K+  +  ++ +
Sbjct: 17   DLKELNKQVSIEEKYNLHGLLGTGAFSEVRLAESKDSPGEHFAVKIIDKKALKGKEESLE 76

Query: 415  NEIGILKM---------------VKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILD 549
            NEI +L+                + HPNI+QL++ +  + + ++ +EL TG E+FD I++
Sbjct: 77   NEIRVLRRFSANHFDGKCLNGTRLTHPNIVQLLETYEDKSKVYLVMELVTGGELFDRIVE 136

Query: 550  QGYYSERDTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE 729
            +G Y+E+D S+++RQ+LEAV Y+H   +VHR+LK ENL+YY+   +SKI+ISDF L+K+E
Sbjct: 137  KGSYTEKDASHLIRQILEAVDYMHEQGVVHRDLKPENLLYYSPDDDSKIMISDFGLSKME 196

Query: 730  N-GLIKEPCGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENH 906
            + G++   CGTP Y+APEV+ ++ YG+ VD W+IGVI YILL G PPFY+E         +
Sbjct: 197  DSGIMATACGTPGYVAPEVLAQKPYGKAVDVWSIGVISYILLCGYPPFYDE--------N 248

Query: 907  DKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAAS 1086
            D NLF +IL GD+EFDSPYWD+IS++AK  +  LM V  ++R T ++A+ H WISGN AS
Sbjct: 249  DANLFAQILKGDFEFDSPYWDEISESAKHFIKNLMCVTVEKRYTCKQALGHAWISGNEAS 308

Query: 1087 DKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAA----QSASATDTATP 1254
             +NI   V  Q++KNFA+++WK+A     T++++++     +S + A      ++S  D+ TP
Sbjct: 309  SRNIHGTVSEQLKKNFAKSRWKQAYYAATVIRQMQRMALNSNSNANFDSSNSSNQDSTTP 368

Query: 1255 GAAGGATAAAASGATSAPEGDAARAAKS 1338
              AA GA  +    + + + A    KS
Sbjct: 369  TAATGAWTSNVLSSQQSVQSHAQEMNKS 396


>gi|4007153|emb|CAA19296.1| (AL023754) dJ272L16.1 (Rat Ca2+/Calmodulin
          dependent Protein Kinase LIKE protein) [Homo sapiens]
          Length = 460

 Score =  286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q + +   +   +V+ +  F E+F  K + TGKL   K  +K   +  + + +NEI +LK
Sbjct: 15   QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 73
```

FIGURE 2G

```
Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
            +KH NI+ L D++ +   Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
Sbjct: 74   KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKY 133

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVVGR 792
            LH   IVHR+LK ENL+Y    +NSKI+I+DF L+K+E NG++   CGTP Y+APEV+ +
Sbjct: 134  LHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 193

Query: 793  QRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDD 972
            + Y + VDCW+IGVI YILL G PPFYEE E          LF KI  G YEF+SP+WDD
Sbjct: 194  KPYSKAVDCWSIGVITYILLCGYPPFYEETE--------SKLFEKIKEGYYEFESPFWDD 245

Query: 973  ISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWK 1152
            IS++AKD +  L+E + ++R T E+A+SH WI GN A  ++I   V  QI+KNFA++KW+
Sbjct: 246  ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 305

Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
            +A     ++  +R    + S                T  +     ++    T AP  D +
Sbjct: 306  QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 365

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
            A +    P      P   G  S     +GS+      S+ P   GS+
Sbjct: 366  ALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 411


>gi|4678722|emb|CAB41259.1| (AL049688) hypothetical protein [Homo
          sapiens]
        Length = 481

 Score =  286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q + +   +  +V+ +  F E+F  K + TGKL   K  +K     +  + +NEI +LK
Sbjct: 20   QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 78

Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
            +KH NI+ L D++ +   Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
Sbjct: 79   KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKY 138

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVVGR 792
            LH   IVHR+LK ENL+Y    +NSKI+I+DF L+K+E NG++   CGTP Y+APEV+ +
Sbjct: 139  LHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 198

Query: 793  QRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDD 972
            + Y + VDCW+IGVI YILL G PPFYEE E          LF KI  G YEF+SP+WDD
Sbjct: 199  KPYSKAVDCWSIGVITYILLCGYPPFYEETE--------SKLFEKIKEGYYEFESPFWDD 250

Query: 973  ISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWK 1152
            IS++AKD +  L+E + ++R T E+A+SH WI GN A  ++I   V  QI+KNFA++KW+
Sbjct: 251  ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 310

Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
            +A     ++  +R    + S                T  +     ++    T AP  D +
Sbjct: 311  QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 370
```

FIGURE 2H

```
Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
            A +    P      P   G  S     +GS+      S+ P   GS+
Sbjct: 371  ALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 416
```

```
>gi|2143639|pir||I56542 calmodulin-binding protein - rat
 gb|AAA16633.1| (L22557) calmodulin-binding protein [Rattus norvegicus]
          Length = 504

 Score =  929 bits (2375), Expect = 0.0
 Identities = 468/509 (91%), Positives = 473/509 (91%), Gaps = 8/509 (1%)
 Frame = +1

Query: 211  MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 390
            MPFGCVTLGDKKNYNQPSEVTDRYDLGQV+KTEEFCEIFRAKDKTTGKLHTCKKFQKRDG
Sbjct: 1    MPFGCVTLGDKKNYNQPSEVTDRYDLGQVVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 60

Query: 391  RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
            RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61   RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 750
            DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP
Sbjct: 121  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 180

Query: 751  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
            CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI
Sbjct: 181  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 240

Query: 931  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 1110
            LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV
Sbjct: 241  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 300

Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAAQSASATDTATPGAAGGATAAAAS 1290
            CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQS TAA      +D ATPGAAGGA AAAA
Sbjct: 301  CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSGTAA-----TSDAATPGAAGGAVAAAAG 355

Query: 1291 G--------ATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITP 1446
            G        AT    GDA  AAKSD++A ADRSATPATDGSATPATDGSVTPATDGSITP
Sbjct: 356  GAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVTPATDGSITP 415

Query: 1447 ATDGSVTPVTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAP 1626
            ATDGSVTP TDRSATPATDGRATPATEESTVP  QSSA  A KAAATPEPA+AQPDSTA
Sbjct: 416  ATDGSVTPATDRSATPATDGRATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTAL 475

Query: 1627 EGATGQAPPSSKGEEAAGYAQESQREEAS 1713
            EGATGQAPPSSKGEEA G AQESQR E S
Sbjct: 476  EGATGQAPPSSKGEEATGCAQESQRVETS 504


 Score = 34.4 bits (77), Expect = 7.1
 Identities = 42/158 (26%), Positives = 60/158 (37%), Gaps = 5/158 (3%)
 Frame = -3

Query: 1673 ASSPLLEGGAWPVAPSGAVLSGWAIA--GSGVAAALVASMALLWVVGTVLSSVAGVALPS 1500
            A++P   GGA   A  GA  +  A A  G+G  A   A          ++S    A P+
Sbjct: 340  AATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAK-------SDDMASADRSATPA 392
```

FIGURE 2I

```
Query: 1499 VAGVALLSVTGVTLPSVAGVMLPSVAGVTLPSVAGVALPSVAGVALRSAGATLSLFAARA 1320
            G A  +  G   P+  G + P+  G   P+    A P+  G
Sbjct: 393  TDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDG---------------R 436

Query: 1319 ASPSGAEVAPLAAAAVAPPAAPGVAV---SVAEADWAA 1215
          A+P+  E    AA + A PAA   A    +VA+ D  A
Sbjct: 437  ATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTA 474


>gi|7521914|pir||T30814 calmodulin-binding protein kinase - Fugu
          rubripes
 emb|CAA09101.1| (AJ010348) calmodulin binding protein kinase [Fugu rubripes]
         Length = 421

 Score =  598 bits (1526), Expect = e-170
 Identities = 296/391 (75%), Positives = 332/391 (84%), Gaps = 2/391 (0%)
 Frame = +1

Query: 211  MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 390
            MPFGC+TLG+KK+YN PSEVTD+YDLGQV+K+EEFCEIFRAKD+ T K++TCKKF K+DG
Sbjct: 1    MPFGCLTLGEKKDYNSPSEVTDKYDLGQVVKSEEFCEIFRAKDRNTLKMYTCKKFNKKDG 60

Query: 391  RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
            RKVRKAAKNEI ILKMVKH NILQLVD F T+KEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61   RKVRKAAKNEIMILKMVKHHNILQLVDAFETKKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571  DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 750
            DTSNV+RQVLEAVAYLHSLKIVHRNLK  NLVY+NRLK+SKIVISDF LAKLENGLIK+P
Sbjct: 121  DTSNVMRQVLEAVAYLHSLKIVHRNLK--NLVYFNRLKHSKIVISDFQLAKLENGLIKDP 178

Query: 751  CGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
            CGTPEYLAPEV+GRQRYGRPVDCWAIGVIMYILLSGNPPFY++ +E+D ++ DKNLF KI
Sbjct: 179  CGTPEYLAPEVIGRQRYGRPVDCWAIGVIMYILLSGNPPFYDDGDEEDSDSRDKNLFLKI 238

Query: 931  LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGV 1110
            L+GDYEFDSPYWDDIS +AK LV  LMEV+QDQR+TA+EAI+HEWISGNAASDKNIKDGV
Sbjct: 239  LSGDYEFDSPYWDDISDSAKTLVASLMEVDQDQRLTAQEAIAHEWISGNAASDKNIKDGV 298

Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAAQSASAT--DTATPGAAGGATAAA 1284
            CAQIEKNFA+AKWKKAVRVTTLMKRLRA EQ  T A+  A+          P   GG+  AA
Sbjct: 299  CAQIEKNFAKAKWKKAVRVTTLMKRLRASEQGDTGASGLAAGATGGPPDPNMPGGSLLAA 358

Query: 1285 ASGATSAPEGDAARAAKSDNVAPADRSATPA 1377
                     + + A S+  A A  S  P+
Sbjct: 359  ----------SIKTALSEKAADAQTSTIPS 378


>gi|3122310|sp|Q63450|KCC1_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN
          KINASE TYPE I (CAM KINASE I)
 pir||S50193 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 gb|AAA66944.1| (L26288) CaM-like protein kinase [Rattus norvegicus]
 prf||2024225A Ca/calmodulin protein kinase I [Rattus norvegicus]
         Length = 374

 Score =  310 bits (787), Expect = 4e-83
 Identities = 156/357 (43%), Positives = 226/357 (62%), Gaps = 4/357 (1%)
 Frame = +1
```

FIGURE 2J

```
Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+        + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +    ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLRAPE--QSSTAAAQSASATDTATPGAAGGATAAAASGATSAP 1308
            KWK+A   T +++ +R  +   S     Q+AS  + TP A G A           P
Sbjct: 302  KWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTPTAGGPAAGCCCRDCCVEP 358


>gi|4502553|ref|NP_003647.1| calcium/calmodulin-dependent protein
          kinase I [Homo sapiens]
 sp|Q14012|KCC1_HUMAN CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (CAM KINASE I)
 pir||S57347 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
 gb|AAA99458.1| (L41816) cam kinase I [Homo sapiens]
        Length = 370

 Score =  309 bits (784), Expect = 9e-83
 Identities = 156/357 (43%), Positives = 225/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+        + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +    ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+    ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301
```

FIGURE 2K

```
Query: 1144 KWKKAVRVTTLMKRLRAPE--QSSTAAAQSASATDTATPGAAGGATAAAASGATSAP 1308
            KWK+A   T +++ +R  +   S     Q+AS  +  TP A G A           P
Sbjct: 302  KWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTPVAGGPAAGCCCRDCCVEP 358


>gi|3114436|pdb|1A06|    Calmodulin-Dependent Protein Kinase From Rat
          Length = 332

 Score =  303 bits (768), Expect = 7e-81
 Identities = 146/316 (46%), Positives = 213/316 (67%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+        + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +     ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+   ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLR 1191
            KWK+A   T +++ +R
Sbjct: 302  KWKQAFNATAVVRHMR 317


>gi|406113|gb|AAA19670.1| (L24907) protein kinase I [Rattus
           norvegicus]
          Length = 332

 Score =  299 bits (758), Expect = 1e-79
 Identities = 146/316 (46%), Positives = 212/316 (66%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250  YNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
            + Q  ++ D YD   V+ T  F E+  A+DK T KL   K   K+        + +NEI +
Sbjct: 10   WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430  LKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAV 609
            L  +KHPNI+ L D++ +     ++ ++L +G E+FD I+++GYY+ERD S ++ QVL+AV
Sbjct: 70   LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGYYTERDASRLIFQVLDAV 129

Query: 610  AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
             YLH L IVHR+LK ENL+YY+  ++SKI+ISDF L+K+E+   ++  CGTP Y+APEV
Sbjct: 130  KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189
```

FIGURE 2L

```
Query: 784  VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
            + ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPY
Sbjct: 190  LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDAKLFEQILKAEYEFDSPY 241

Query: 964  WDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
            WDDIS +AKD +  LME + ++R T E+A+ H WI+G+ A DKNI   V  QI+KNFA++
Sbjct: 242  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLR 1191
            KWK+A   T +++ +R
Sbjct: 302  KWKQAFNRTAVVRHMR 317


>gi|9966875|ref|NP_065130.1| CamKI-like protein kinase [Homo sapiens]
 gb|AAG00534.1|AF286366_1 (AF286366) CamKI-like protein kinase [Homo sapiens]
          Length = 357

 Score =  299 bits (757), Expect = 1e-79
 Identities = 142/332 (42%), Positives = 221/332 (65%), Gaps = 2/332 (0%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q  ++   ++  + + T  F E+  A++K TGKL   K   K+  +    + +NEI +L+
Sbjct: 15   QAEDIKKIFEFKETLGTGAFSEVVLAEEKATGKLFAVKCIPKKALKGKESSIENEIAVLR 74

Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
             +KH NI+ L D++ +     ++ ++L +G E+FD I+++G+Y+E+D S ++RQVL+AV Y
Sbjct: 75   KIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAVYY 134

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE--NGLIKEPCGTPEYLAPEVVG 789
            LH + IVHR+LK ENL+YY++ + SKI+ISDF L+K+E     ++  CGTP Y+APEV+
Sbjct: 135  LHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVLA 194

Query: 790  RQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWD 969
            ++ Y + VDCW+IGVI YILL G PPFY+E          +D  LF +IL  +YEFDSPYWD
Sbjct: 195  QKPYSKAVDCWSIGVIAYILLCGYPPFYDE--------NDSKLFEQILKAEYEFDSPYWD 246

Query: 970  DISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKW 1149
            DIS +AKD +  LME + ++R T E+A  H WI+G+ A +KNI + V AQI KNFA++KW
Sbjct: 247  DISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKW 306

Query: 1150 KKAVRVTTLMKRLRAPEQSSTAAAQSASATDT 1245
            ++A   T +++ +R     S+  + +AS + +
Sbjct: 307  RQAFNATAVVRHMRKLHLGSSLDSSNASVSSS 338


>gi|3893099|emb|CAA76937.1| (Y17917) calcium/calmodulin dependent
          protein kinase I [Drosophila melanogaster]
 gb|AAF59343.1| (AE003844) CaMKI gene product [alt 2] [Drosophila melanogaster]
          Length = 405

 Score =  288 bits (729), Expect = 3e-76
 Identities = 152/388 (39%), Positives = 243/388 (62%), Gaps = 21/388 (5%)
 Frame = +1
```

FIGURE 2M

```
Query: 238  DKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTT-GKLHTCKKFQKRDGRKVRKAAK 414
            D K  N+   + ++Y+L  ++ T  F E+  A+ K + G+     K   K+  +   ++ +
Sbjct: 17   DLKELNKQVSIEEKYNLHGLLGTGAFSEVRLAESKDSPGEHFAVKIIDKKALKGKEESLE 76

Query: 415  NEIGILKM--------------VKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILD 549
            NEI +L+                + HPNI+QL++ +  + + ++ +EL TG E+FD I++
Sbjct: 77   NEIRVLRRFSANHFDGKCLNGTRLTHPNIVQLLETYEDKSKVYLVMELVTGGELFDRIVE 136

Query: 550  QGYYSERDTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE 729
            +G Y+E+D S+++RQ+LEAV Y+H    +VHR+LK ENL+YY+    +SKI+ISDF L+K+E
Sbjct: 137  KGSYTEKDASHLIRQILEAVDYMHEQGVVHRDLKPENLLYYSPDDDSKIMISDFGLSKME 196

Query: 730  N-GLIKEPCGTPEYLAPEVVGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENH 906
            + G++   CGTP Y+APEV+ ++ YG+ VD W+IGVI YILL G PPFY+E         +
Sbjct: 197  DSGIMATACGTPGYVAPEVLAQKPYGKAVDVWSIGVISYILLCGYPPFYDE--------N 248

Query: 907  DKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAAS 1086
            D NLF +IL GD+EFDSPYWD+IS++AK  +  LM V  ++R T ++A+ H WISGN AS
Sbjct: 249  DANLFAQILKGDFEFDSPYWDEISESAKHFIKNLMCVTVEKRYTCKQALGHAWISGNEAS 308

Query: 1087 DKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAA----QSASATDTATP 1254
             +NI   V  Q++KNFA+++WK+A    T++++++    +S + A     ++S  D+ TP
Sbjct: 309  SRNIHGTVSEQLKKNFAKSRWKQAYYAATVIRQMQRMALNSNSNANFDSSNSSNQDSTTP 368

Query: 1255 GAAGGATAAAASGATSAPEGDAARAAKS 1338
            AA GA  +    + + + A    KS
Sbjct: 369  TAATGAWTSNVLSSQQSVQSHAQEMNKS 396


>gi|4007153|emb|CAA19296.1| (AL023754) dJ272L16.1 (Rat Ca2+/Calmodulin
          dependent Protein Kinase LIKE protein) [Homo sapiens]
        Length = 460

 Score =  286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q + +   +   +V+ +  F E+F  K + TGKL    K  +K     +  + +NEI +LK
Sbjct: 15   QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 73

Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
             +KH NI+ L D++ +   Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
Sbjct: 74   KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKY 133

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVVGR 792
            LH   IVHR+LK ENL+Y    +NSKI+I+DF L+K+E NG++   CGTP Y+APEV+ +
Sbjct: 134  LHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 193

Query: 793  QRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDD 972
            + Y + VDCW+IGVI YILL G PPFYEE E              LF KI  G YEF+SP+WDD
Sbjct: 194  KPYSKAVDCWSIGVITYILLCGYPPFYEETE--------SKLFEKIKEGYYEFESPFWDD 245

Query: 973  ISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWK 1152
            IS++AKD +  L+E + ++R T E+A+SH WI GN A  ++I    V  QI+KNFA++KW+
Sbjct: 246  ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 305
```

FIGURE 2N

```
Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
            +A     ++  +R     +  S                  T  +      ++      T AP   D +
Sbjct: 306  QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 365

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
            A  +    P       P   G  S      +GS+       S+ P    GS+
Sbjct: 366  ALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 411


>gi|4678722|emb|CAB41259.1| (AL049688) hypothetical protein [Homo
          sapiens]
         Length = 481

 Score =  286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256  QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
            Q + +    +   +V+ +  F E+F   K + TGKL    K  +K     +   + +NEI +LK
Sbjct: 20   QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 78

Query: 436  MVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVVRQVLEAVAY 615
             +KH NI+ L D++ +    Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
Sbjct: 79   KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKY 138

Query: 616  LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVVGR 792
            LH   IVHR+LK ENL+Y    +NSKI+I+DF L+K+E NG++   CGTP Y+APEV+ +
Sbjct: 139  LHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 198

Query: 793  QRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDD 972
            + Y + VDCW+IGVI YILL G PPFYEE E          LF KI  G YEF+SP+WDD
Sbjct: 199  KPYSKAVDCWSIGVITYILLCGYPPFYEETE--------SKLFEKIKEGYYEFESPFWDD 250

Query: 973  ISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWK 1152
            IS++AKD +  L+E + ++R T E+A+SH WI GN A  ++I   V  QI+KNFA++KW+
Sbjct: 251  ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 310

Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
            +A     ++  +R     +  S                  T  +      ++      T AP   D +
Sbjct: 311  QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 370

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
            A  +    P       P   G  S      +GS+       S+ P    GS+
Sbjct: 371  ALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 416
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	229.1	6.5e-65	1
CE00022	CE00022 MAGUK_subfamily_d	105.3	5.5e-31	2
CE00287	CE00287 PTK_Eph_orphan_receptor	-71.4	0.0011	1
CE00292	CE00292 PTK_membrane_span	-87.6	0.00079	1
CE00291	CE00291 PTK_fgf_receptor	-125.1	0.13	1
CE00286	E00286 PTK_EGF_receptor	-159.5	0.3	1
CE00290	CE00290 PTK_Trk_family	-188.3	0.028	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-237.5	0.0016	1

FIGURE 20

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
CE00022	1/2	117	152	..	118	153	..	4.3	0.35
CE00286	1/1	43	245	..	1	263	[]	-159.5	0.3
CE00292	1/1	26	259	..	1	288	[]	-87.6	0.00079
CE00290	1/1	29	266	..	1	282	[]	-188.3	0.028
CE00291	1/1	24	266	..	1	285	[]	-125.1	0.13
CE00287	1/1	24	284	..	1	260	[]	-71.4	0.0011
PF00069	1/1	37	286	..	14	278	.]	229.1	6.5e-65
CE00022	2/2	182	286	..	188	283	..	100.8	1.2e-29
CE00016	1/1	3	357	..	1	433	[]	-237.5	0.0016

FIGURE 2P

```
   1 AATGAAATCC TGTATCTACA AAAAAATTTT TAAAAATTAG CCAGTTGTGG
  51 TGGTGTGCAC CTATGGTCCA GTCCTAGCTA CTCAGGAGGC TGAGGTGGGA
 101 GGATCGCTTG AGCCCAGGAG GTTGAGGCTG GAATGAGCTG TGATCATTCC
 151 ACTGCATTCC AGCCTGGGTG CCACTGCATT CCAGCCTGGG TGACAGAACA
 201 GCTGGGCATG GTGCGGGTGC CTGTAATCCC AGCTGCGGTG GGAGGATCGT
 251 TTGAGTTCAG GAGCTCTGGG CTGCAGTGCG CTATGCCAGT TGGGTGTCTA
 301 CACTAAGTTT GGCATTAGTA TGGTGACTTC CTGGGAGCTA GAGCTCATCA
 351 GGTTGCCTAA AGGAGGGGTG AAGCAACCAA GGTCAGAGAC GAAGCAGGTC
 401 AAAACTCCTG TGCTGATCAG TAGTGGGCTT GTGCCCATGA ATAGCCACTG
 451 CACTCCAGCC TGGGCAACAT AGTGAGACTT GTCTCTAAAA AAAGAAAGAA
 501 AGAAAGAAAA GAAAAGAAAA GAAATAGGTC TTCCAGAATC CCCCCCATGT
 551 GTCCTGAATC AATCATAACC CCTCCTTTTC TCTTAGAAGG GACCATTATC
 601 TGACTCTGCT TATTTCCTAG CTTTTCTTTA TAGCTCTACT GCTGTGTTTG
 651 TATCCCCCTT ACGGGTTTGT TCTGCCTGTT TGAACTCTAT CAATAGACTC
 701 ATACTATATG TATTCTTTTG TGTCTTTTTG CACTTAACAC TGTGTAAGAG
 751 TCACCAGGTG GTTGGGTATA GCTGTAGCTC CTTTGTTTCC ATTGCTATAT
 801 AATATTCCAT TGTGTGACTC TACCACAATA CATCCTGTTG GTGGTGGTAT
 851 TTGGTCTGTT TTCAATTTTT GGCGATTATG TATATGGCTA CTATGAGCAT
 901 TGTATGACTG TCCTGATGCA CGAATATGTG CACTTCTGTA GGCACGTATT
 951 TAGGAGTGCA ATTGCTGGTT CATAGGGTAT GTTTGTTTGA CTTTAGTGGT
1001 TTTACCAAAC TGCTTTACAA AGGGGAGTTT GCCCTCTCCT AGCAGTGCTC
1051 ACGTTCTTCA TATATCCACT AACACTTGTT AGCTCTAGAC CTTCAGAGAT
1101 GACTAGCAGG TGGGTGGGTG GTTATAGCCC CCTTCATCTG TAAAATAGCT
1151 GAAATTTAAA TAAACTGTTT GATAAGCCTT TTTTTGAATG TATAGAATAC
1201 AAAACTATTC CCTTATATAT CAGCTTAATA CATTTTTTCA TATGTAGGCT
1251 GTTGCACTTC AGGCAGCCAA GCTGAGTAGC TGGATGTCTA GCCAGAAAAG
1301 CAGGGGTAGG ATCTAAGCCT GCCTATCCTC TAGCCCCTCC TGGTATGGTC
1351 TCTGCCCCTA GCTTGGCCTG AGCCAGGTTG GGGTCTCCCA AAAGCAGCCC
1401 CTATGTTGTG GGGAAGTGGA GAGTAGTACA GCTAAGCCAG ACCCCATTGT
1451 GCCCGCAGGT TAGAGCCTGG CAATGCCGTT TGGGTGTGTG ACTCTGGGCG
1501 ACAAGAAGAA CTATAACCAG CCATCGGAGG TGACTGACAG ATATGATTTG
1551 GGACAGGTCA TCAAGACGTG AGTGCCGGGC CTGTCAGGCA AGGCTGGGTG
1601 GGCTGGTGAG CAGGGGCTAG GGAAGTGGCA GTGGAGTGCA GCTGATGCTA
1651 AGGCCAGGCC TGAGTGGGTG CCTGTCGGCT GCAGTGAGGA GTTTTGTGAA
1701 ATCTTCCGGG CCAAGGACAA GACGACAGGC AAGCTGCACA CCTGCAAGAA
1751 GTTCCAGAAG CGGGACGGCC GCAAGGTGCG GAAAGCTGCC AAGAACGAGA
1801 TAGGCATCCT CAAGATGTGA GTTTGAGGCC TGGGATTGGG GCGGGGTGGG
1851 AGGCAGCAGG GAAGGGCTTA GAGGGCAAGT GGCCTCAGGC AGTCCCAGCC
1901 TCTGGCCAAT TAGTACTGCT GTGGCCACTG TGGTGACCAC AGCCTCTCCC
1951 AGGGGTTCAT CCAGCCCTAA CTACTGGCTC CCCTCCCTGT CGCCAGGGTG
2001 AAGCATCCCA ACATCCTACA GCTGGTGGAT GTGTTTGTGA CCCGCAAGGA
2051 GTACTTTATC TTCCTGGAGC TGTGAGTGTG GGTCTGGGGA CCCAAGATTC
2101 CCCAGCGCCC AGGGCTTTCA CCTGTCCCAC CCTCTGCAGC TAAGGAAACC
2151 CCCTTTCTGG ACCCTTGGCG TCCCAGGTCC CTGTGCCTTG CTCAGCCAGC
2201 TGCCTGGCGT AGGCAGCTCA CCCAAGTGCT CCTGCCCTAC CCCTGATTCT
2251 GCCCACGCCA GGCTCAGGGG CTGGTGTCCC TCAGGGCCAC GGGGAGGGAG
2301 GTGTTTGACT GGATCCTGGA CCAGGGCTAC TACTCGGAGC GAGACACAAG
2351 CAACGTGGTA CGGCAAGTCC TGGAGGCCGT GGCCTATTTG CACTCACTCA
2401 AGATCGTGCA CAGGAATCTC AAGGTGAGGG CAGAGCCAGA GTCAAAGGGC
2451 CAGTTGGCAG CTGGGCTGGT GCTGGGGTGG GCAGCACCTC AGGGCCTTGG
2501 TCTAGCCTCC AAGGTCCTCA TGGTGTCTTC TGCTCACCCA CATGCTATTC
2551 TCACACCACA GCTGGAGAAC CTGGTTTACT ACAACCGGCT GAAGAACTCG
2601 AAGATTGTCA TCAGTGACTT CCATCTGGCT AAGCTAGAAA ATGGCCTCAT
2651 CAAGGAGCCC TGTGGGACCC CCGAGTATCT GGGCAAGCAG GGGGTGGGGC
2701 AGGGGCAGGG GGATAATGGG GGGCAGCCTT CAGGGAGCTG CTCTGGGCAG
2751 GGGGAAAATG TGCTCATCTC AGGAAGCTGG TGTGGATGGT ACTGGACCTG
2801 GCTAGGCCTG ATACTGACCA GCAGATGGGC GCTGTGTTTG TAGCCCCAGA
2851 GGTGGTAGGC CGGCAGCGGT ATGGACGCCC TGTGGACTGC TGGGCCATTG
2901 GAGTCATCAT GTACATCCTG TGAGTGGACA GATGGACAAG CAGGCTTGCA
```

FIGURE 3A

2951 GTCAGATGGG GTGGGGGCAT GTGTCTGTGG CCTTTCTGTG TGACCCTTCC
3001 CCCATGCAGG CTTTCAGGCA ACCCACCTTT CTATGAGGAG GTGGAAGAAG
3051 ATGATTATGA GAACCATGAT AAGAATCTCT TCCGCAAGAT CCTGGCTGGT
3101 GACTATGAGT TTGACTCTCC ATATTGGGAT GATATTTCGC AGGCAGGTGA
3151 GGAGGTGCCT GCCCAGCACT TGGTAGAACG CAAGGGAGTG GGGAGGGTGT
3201 CCTGCTCTCA TCTTCCTCTG TGGTATTCTG CTTCTGTCCC CCAGCCCATT
3251 TATCACCTCT AGACATTGAG ATGGGGTGCC CATGACTATC CCCTCCTTGG
3301 TTTTGTCCAC AGCCAAAGAC CTGGTCACAA GGCTGATGGA GGTGGAGCAA
3351 GACCAGCGGA TCACTGCAGA AGAGGCCATC TCCCATGAGT GGTGAGCAGG
3401 GTCCAGGGGA GGGTGGGAGA GGCCAGGGTC CCCCTCACAC CCAGCAGCCC
3451 CATCTTTGAG GCCTAGAAGG GGTGCAGGTA CCTAGAGCTC AGGGCAGCCC
3501 AGAGGCTCTG CCTGGTAGTC CCTGGATGCC ACATAGAAGG GCTGAGCAGA
3551 GTCTCCACAA AGGCTCATTC TCTCAGATCC AGACACACTT GCACCCTTTC
3601 CAGGATTTCT GGCAATGCTG CTTCTGATAA GAACATCAAG GATGGTGTCT
3651 GTGCCCAGAT TGAAAAGAAC TTTGCCAGGG CCAAGTGGAA GGTAAGGCTT
3701 GGATAACTCC CTTCTTGGCT CTATCCCAAG TATTGCTTCT GGCACTCAGT
3751 TTCTTGCCTG CATCACACCC CTGCAGCCAC ACACAAGCTT TTCTCAGGCC
3801 ATCAGGTGTG GGTGTAGCCA CTGTGATTAC CTTAAGTAGG AGTGCTGAGC
3851 AGCTGAGTAC TTGGCCCTGG GGTGGATGGA GGTGGCCGGG GGTACTATGG
3901 AAGGAGTTTG GTTTGGTCAC TGCCAAGCAA TGGATCCAGC AAGCCTCACC
3951 CTTAGCCTTT CTCCACTGTG CTCCTTTCAG AAGGCTGTCC GAGTGACCAC
4001 CCTCATGAAA CGGCTCCGGG CACCAGAGCA GTCCAGCACG GCTGCAGCCC
4051 AGTCGGCCTC AGCCACAGAC ACTGCCACCC CCGGGGCTGC AGGTGGGGCC
4101 ACAGCTGCAG CTGCGAGTGG AGCTACCTCA GCCCCTGAGG GTGATGCTGC
4151 TCGTGCTGCA AAGAGTGATA ATGTGGCCCC CGCAGACCGT AGTGCCACCC
4201 CAGCCACAGA TGGAAGTGCC ACCCCAGCCA CTGATGGCAG TGTCACCCCA
4251 GCCACCGATG GAAGCATCAC TCCAGCCACT GATGGGAGTG TCACCCCAGC
4301 CACTGACAGG AGCGCTACTC CAGCCACTGA TGGGAGAGCC ACACCAGCCA
4351 CAGAAGAGAG CACTGTGCCC ACCACCCAAA GCAGTGCCAT GCTGGCCACC
4401 AAGGCAGCTG CCACCCCTGA GCCGGCTATG GCCCAGCCGG ACAGCACAGC
4451 CCCAGAGGGC GCCACAGGCC AGGCTCCACC CTCTAGTAAA GGGGAAGAGG
4501 CTGCTGGTTA TGCCCAGGAG TCTCAAAGGG AGGAGGCCAG CTGAGTAGGC
4551 AGCCTGGTGA GGGGGGGCAG GGGATGGGCA GGAGGGTGGG AGAGTGGATG
4601 AGGGGCTTCT CACTGTACAT AGAGTCACTG GCATGATGCC CTCGCTCCCC
4651 CATGCCCCCA CATCCCAGTG GGGCATAACT AGGGGTCACG GGAGAGCAGT
4701 CTCGTCTCCT GTGTGTATGT GTGTGAGTGG TGGGCAGGCC AGTGGCAGGG
4751 CCGGCCCCAG CCCCTGCATG GATTCCTTGT GGCTTTTCTG TCTTTTGCTA
4801 GCTTCACCAG TTTCTGTTCC TTGTGGGATG CTGCTCTAGG GATACTCAGG
4851 GGGCTCCTGC TCTCCTTCCC CTTCCCTTCT TGCCTCACCA TTCCCCTAGG
4901 CAGGCCCTGC AGGTCCCACA CTCTCCCAGG CCCTAAACTT GGGCGGCCTT
4951 GCCCTGAGAG CTGGTCCTCC AGCGAGGCCC TGTCAGCGGT CTTAGGCTCC
5001 TGCACATGAA GGTGTGTGCC TGTGGTGTGT GGGCTGCTCT AGGAGCAGAT
5051 ACAGGCTGGT ATAGAGGATG CAGAAAGGTA GGGCAGTATG TTTAAGTCCA
5101 GACTTGGCAC ATGGCTAGGG ATACTGCTCA CTAGCTGTGG AGGTCCTCAG
5151 GAGTGGAGAG AATGAGTAGG AGGGCAGAAG CTTCCATTTT TGTCCTTCCT
5201 AAGACCCTGT TATTTGTGTT ATTTCCTGCC TTTCCGAGTC CTGCAGTGGG
5251 CTGCCCTGTA CCCTGAACCT CATGAGCCTC TAAGGGAAAG GAGGAACAAT
5301 TAGGACGTGG CAATGAGACC TGGCAGGGCA GAGTACAAGC CCAGCACCCA
5351 GTGTCCCAGC CTTAATGGGT CCTTACCATG GGCCAAACAG GGAGGGCTGA
5401 TACCTCCTTG CTCTTCCTAG ATGCCCACCT CCTACAATCT CAGCCCACAA
5451 GTCCTCTCCA CCTAGGGGGC TTGCTGCATG GCAATAACTC ATAATTTGAT
5501 TTGGAGGTTT GCCCTTTACA GGGGCAGATT TTCTGCTCAG TTCAACAATG
5551 AAATGAAGAG GAACTCCCTC TTTCTACAGC TCACTTCTAT CAGAGGCCCA
5601 GGTGCCTCAG AGCCACATTG AGTTGCTTTT TCTGGGATGA GGAAGTAGGG
5651 TTAAACTCCC CAGTTTCCTG AGGGAGGCTC CTGACAGGTG CCCTTTGTCA
5701 GACCCTACCA CAGCCTGGAT AGGCAGCCAC ATTGGTCCTC GCCCTTGCTC
5751 GGCACTCCGT GGTGGTCCTG CCCTTCTCCC TGCATGCCTG TGGGTCTGCT
5801 CTGGTGTGTG AAGGTCGGTG GGTTAACTGT GTGCCTACTG AACCTGGCAA
5851 ATAAACATCA CCCTGCAAAG CCTCTGGCCA CCCTCTCGCC TTTGCTTCCT

FIGURE 3B

```
5901 CTGTCCTACT GGGGAGGAGC CCCTGGAAGG CAGTGGGGAA GGGAGAGGCT
5951 GGGAGCAGGT TCACAAGTAG TGGCTGGGAG TAGTAGTGAA CAGTGCCCTG
6001 TGGATTTCTT GGGCTGAGGG TGAAGATCAT CCTCACCACA GTGTATTCCT
6051 CAATGGTGGT GGTGGTGGGG GTCCTCTGAA CTCTAGAAAT CCATGTGAGT
6101 AGTGGGTCTT GGGCTGCATT TGGACCAAGG AATACTCCCT GGGCTGAGAG
6151 CTCAAGTAAG GGCTGCTGTT TTTGACTCCT GTTGACCGAG GAGCCTTACT
6201 CTTGATTTAG GCATAGAGCT GGAATCTACC TGGGCCAGCC AGCGCAAGGA
6251 CAGACCCTGC TCATAGCCAA AGATAGCTTC CCTGAGCTAG GGAGAGGGTG
6301 TAGGGTGAGC AATGCACAAA GATTCTATGC TGCTCTGTGT TGATTCCTTC
6351 TTTCTGTGAA CACCTGTGCT TTCCACCTAT GCCCCAAATG AAATCTCACT
6401 CTGGGTCTAT TTCAGCTGGA GCAGATCAGC TTTATATTAT GGGACTATGC
6451 ACAGGGTTTC TTCTGGGTAG AGGGAGTAAC ACTGCCACAG ATACTAAGCC
6501 TAAAAACCCA AAAGTTGACT TACTCCAGCC CAGGTGGGCC TGGGTGAACT
6551 CACCAGGGAT GCTGCTCTCT GGGAGGACCT CAAAGATAAC CTCCTCAAGG
6601 ATAACTTCTC TGATGTGGGA ATAATAAAAA GGATTTGTTA GTCTCTAGTC
6651 TTTGAAGCAT CTGGGCCTCC AAAATTCCAA CCCTACTACA GTCTCAAGCA
6701 TAACTGATCC TCCTGAGAGC TAAGAGCTAA AGTCAGGGTA CTGGCCCTAG
6751 TGTCTCCAAA CTCAAGGATA GTCATATCTT ACTTGGATGA AGCCAAGGTT
6801 GGCCTGGGGT GACCTGAGGG ACTGGGGCCT ATGTGTCCAT CTTTCTAGAA
6851 TCGCCCGGAA CTGAGGACTG AGAGGGTAGG GTATTGTGGT CTATGGGAAC
6901 TACAGACCAT AGCGCATGGT CCATCACTGT CCAGAGCCCA AGGGACCCAT
6951 CGGGACCATT GTTCTATTCC CTTGCGGCTG CGGTTTTCTC TGCCTTGGCC
7001 CAGCCTGCCT CGCGCCAGCT CTGGCATGGG ACCACAATGC GCTGCCTTGC
7051 CCTGGAAAAG GGTCCAGCTG GCAGCCTCGC TGCTCCCCGC CTTGATATAA
7101 TGCTGCGCTC TCAAGTGGCA GGTCGAGTCT CCCCAGAGGA CGCCTGAGAG
7151 CGACCGCGCT CCGCCCAGGA TTCTCTACGG CCTCGGGGCC GCTAAGCCCC
7201 GCCCATAGTT CCGCCCATCC GAGAATTTGT CCAATCCAGG CGAAGTATTC
7251 ACGCTCCGCC CAAAGTTTTG TGTTGTCACT TCCGGCCCGC TCCAGGAAGT
7301 CGTGCTGCGG AGCCAAATTT GAAGCAAGCG GAGGCGCGGG GGCGCGTCTA
7351 CGAAGCCGGA CCTGTAGCAG TTTCTTTGGC TGCCTGGGCC CCTTGAGTCC
7401 AGCCATCATG CCTATCCGTG CTCTGTGCAC TATCTGCTCC GACTTCTTCG
7451 ATCACTCCCG CGACGTGGCC GCCATCCACT GCGGCCACAC CTTCCACTTG
7501 CAGTGGTGAG TGACTGCAGT GTTGGGGCCC GGTGTTTGCC CG
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FEATURES:

Start:	1473
Exon:	1473-1567
Intron:	1568-1684
Exon:	1685-1816
Intron:	1817-1996
Exon:	1997-2071
Intron:	2072-2284
Exon:	2285-2423
Intron:	2424-2561
Exon:	2562-2682
Intron:	2683-2843
Exon:	2844-2919
Intron:	2920-3009
Exon:	3010-3146
Intron:	3147-3312
Exon:	3313-3391
Intron:	3392-3603
Exon:	3604-3691
Intron:	3692-3980
Exon:	3981-4541
Stop:	4542

FIGURE 3C

CHROMOSOME MAP POSITION:
Bac Accession #: AC068701
Chromosome: 3

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
234	T	A	Beyond ORF(5')			
328	T	C	Beyond ORF(5')			
1499	C	T	Exon	9	G	G
3022	T	C	Exon	217	N	N
3295	C	T	Intron			
4677	T	A	Beyond ORF(3')			
5583	C	T A	Beyond ORF(3')			
6242	G	C	Beyond ORF(3')			
7264	G	A	Beyond ORF(3')			

Context:

DNA Position

234
AATGAAATCCTGTATCTACAAAAAAATTTTTAAAAATTAGCCAGTTGTGGTGGTGTGCAC
CTATGGTCCAGTCCTAGCTACTCAGGAGGCTGAGGTGGGAGGATCGCTTGAGCCCAGGAG
GTTGAGGCTGGAATGAGCTGTGATCATTCCACTGCATTCCAGCCTGGGTGCCACTGCATT
CCAGCCTGGGTGACAGAACAGCTGGGCATGGTGCGGGTGCCTGTAATCCCAGC
[T,A]
GCGGTGGGAGGATCGTTTGAGTTCAGGAGCTCTGGGCTGCAGTGCGCTATGCCAGTTGGG
TGTCTACACTAAGTTTGGCATTAGTATGGTGACTTCCTGGGAGCTAGAGCTCATCAGGTT
GCCTAAAGGAGGGGTGAAGCAACCAAGGTCAGAGACGAAGCAGGTCAAAACTCCTGTGCT
GATCAGTAGTGGGCTTGTGCCCATGAATAGCCACTGCACTCCAGCCTGGGCAACATAGTG
AGACTTGTCTCTAAAAAAAGAAAGAAAGAAAAGAAAAGAAAAGAAATAGGTCTTCC

328
TTTTAAAAATTAGCCAGTTGTGGTGGTGTGCACCTATGGTCCAGTCCTAGCTACTCAGGA
GGCTGAGGTGGGAGGATCGCTTGAGCCCAGGAGGTTGAGGCTGGAATGAGCTGTGATCAT
TCCACTGCATTCCAGCCTGGGTGCCACTGCATTCCAGCCTGGGTGACAGAACAGCTGGGC
ATGGTGCGGGTGCCTGTAATCCCAGCTGCGGTGGGAGGATCGTTTGAGTTCAGGAGCTCT
GGGCTGCAGTGCGCTATGCCAGTTGGGTGTCTACACTAAGTTTGGCATTAGTATGGTGAC
[T,C]
TCCTGGGAGCTAGAGCTCATCAGGTTGCCTAAAGGAGGGGTGAAGCAACCAAGGTCAGAG
ACGAAGCAGGTCAAAACTCCTGTGCTGATCAGTAGTGGGCTTGTGCCCATGAATAGCCAC
TGCACTCCAGCCTGGGCAACATAGTGAGACTTGTCTCTAAAAAAAGAAAGAAAGAAAGAA
AAGAAAAGAAAAGAAATAGGTCTTCCAGAATCCCCCCCATGTGTCCTGAATCAATCATAA
CCCCTCCTTTTCTCTTAGAAGGGACCATTATCTGACTCTGCTTATTTCCTAGCTTTTCTT

1499
ACAAAACTATTCCCTTATATATCAGCTTAATACATTTTTTCATATGTAGGCTGTTGCACT
TCAGGCAGCCAAGCTGAGTAGCTGGATGTCTAGCCAGAAAAGCAGGGGTAGGATCTAAGC
CTGCCTATCCTCTAGCCCCTCCTGGTATGGTCTCTGCCCCTAGCTTGGCCTGAGCCAGGT
TGGGGTCTCCCAAAAGCAGCCCCTATGTTGTGGGGAAGTGGAGAGTAGTACAGCTAAGCC
AGACCCCATTGTGCCCGCAGGTTAGAGCCTGGCAATGCCGTTTGGGTGTGTGACTCTGGG
[C,T]
GACAAGAAGAACTATAACCAGCCATCGGAGGTGACTGACAGATATGATTTGGGACAGGTC
ATCAAGACGTGAGTGCCGGGCCTGTCAGGCAAGGCTGGGTGGGCTGGTGAGCAGGGGCTA
GGGAAGTGGCAGTGGAGTGCAGCTGATGCTAAGGCCAGGCCTGAGTGGGTGCCTGTCGGC
TGCAGTGAGGAGTTTTGTGAAATCTTCCGGGCCAAGGACAAGACGACAGGCAAGCTGCAC
ACCTGCAAGAAGTTCCAGAAGCGGGACGGCCGCAAGGTGCGGAAAGCTGCCAAGAACGAG

3022
GGCAGCCTTCAGGGAGCTGCTCTGGGCAGGGGGAAAATGTGCTCATCTCAGGAAGCTGGT

FIGURE 3D

GTGGATGGTACTGGACCTGGCTAGGCCTGATACTGACCAGCAGATGGGCGCTGTGTTTGT
AGCCCCAGAGGTGGTAGGCCGGCAGCGGTATGGACGCCCTGTGGACTGCTGGGCCATTGG
AGTCATCATGTACATCCTGTGAGTGGACAGATGGACAAGCAGGCTTGCAGTCAGATGGGG
TGGGGGCATGTGTCTGTGGCCTTTCTGTGTGACCCTTCCCCCATGCAGGCTTTCAGGCAA
[T,C]
CCACCTTTCTATGAGGAGGTGGAAGAAGATGATTATGAGAACCATGATAAGAATCTCTTC
CGCAAGATCCTGGCTGGTGACTATGAGTTTGACTCTCCATATTGGGATGATATTTCGCAG
GCAGGTGAGGAGGTGCCTGCCCAGCACTTGGTAGAACGCAAGGGAGTGGGGAGGGTGTCC
TGCTCTCATCTTCCTCTGTGGTATTCTGCTTCTGTCCCCCAGCCCATTTATCACCTCTAG
ACATTGAGATGGGGTGCCCATGACTATCCCCTCCTTGGTTTTGTCCACAGCCAAAGACCT

3295 CCTTCCCCCATGCAGGCTTTCAGGCAACCCACCTTTCTATGAGGAGGTGGAAGAAGATGA
TTATGAGAACCATGATAAGAATCTCTTCCGCAAGATCCTGGCTGGTGACTATGAGTTTGA
CTCTCCATATTGGGATGATATTTCGCAGGCAGGTGAGGAGGTGCCTGCCCAGCACTTGGT
AGAACGCAAGGGAGTGGGGAGGGTGTCCTGCTCTCATCTTCCTCTGTGGTATTCTGCTTC
TGTCCCCCAGCCCATTTATCACCTCTAGACATTGAGATGGGGTGCCCATGACTATCCCCT
[C,T]
CTTGGTTTTGTCCACAGCCAAAGACCTGGTCACAAGGCTGATGGAGGTGGAGCAAGACCA
GCGGATCACTGCAGAAGAGGCCATCTCCCATGAGTGGTGAGCAGGGTCCAGGGGAGGGTG
GGAGAGGCCAGGGTCCCCCTCACACCCAGCAGCCCCATCTTTGAGGCCTAGAAGGGGTGC
AGGTACCTAGAGCTCAGGGCAGCCCAGAGGCTCTGCCTGGTAGTCCCTGGATGCCACATA
GAAGGGCTGAGCAGAGTCTCCACAAAGGCTCATTCTCTCAGATCCAGACACACTTGCACC

4677 CAAAGCAGTGCCATGCTGGCCACCAAGGCAGCTGCCACCCCTGAGCCGGCTATGGCCCAG
CCGGACAGCACAGCCCCAGAGGGCGCCACAGGCCAGGCTCCACCCTCTAGTAAAGGGGAA
GAGGCTGCTGGTTATGCCCAGGAGTCTCAAAGGGAGGAGGCCAGCTGAGTAGGCAGCCTG
GTGAGGGGGGGCAGGGGATGGGCAGGAGGGTGGGAGAGTGGATGAGGGGCTTCTCACTGT
ACATAGAGTCACTGGCATGATGCCCTCGCTCCCCCATGCCCCCACATCCCAGTGGGGCAT
[T,A]
ACTAGGGGTCACGGGAGAGCAGTCTCGTCTCCTGTGTGTATGTGTGTGAGTGGTGGGCAG
GCCAGTGGCAGGGCCGGCCCCAGCCCCTGCATGGATTCCTTGTGGCTTTTCTGTCTTTTG
CTAGCTTCACCAGTTTCTGTTCCTTGTGGGATGCTGCTCTAGGGATACTCAGGGGCTCC
TGCTCTCCTTCCCCTTCCCTTCTTGCCTCACCATTCCCCTAGGCAGGCCCTGCAGGTCCC
ACACTCTCCCAGGCCCTAAACTTGGGCGGCCTTGCCCTGAGAGCTGGTCCTCCAGCGAGG

5583 AGGGAAAGGAGGAACAATTAGGACGTGGCAATGAGACCTGGCAGGGCAGAGTACAAGCCC
AGCACCCAGTGTCCCAGCCTTAATGGGTCCTTACCATGGGCCAAACAGGGAGGGCTGATA
CCTCCTTGCTCTTCCTAGATGCCCACCTCCTACAATCTCAGCCCACAAGTCCTCTCCACC
TAGGGGGCTTGCTGCATGGCAATAACTCATAATTTGATTTGGAGGTTTGCCCTTTACAGG
GGCAGATTTTCTGCTCAGTTCAACAATGAAATGAAGAGGAACTCCCTCTTTCTACAGCTC
[C,T,A]
CTTCTATCAGAGGCCCAGGTGCCTCAGAGCCACATTGAGTTGCTTTTTCTGGGATGAGGA
AGTAGGGTTAAACTCCCCAGTTTCCTGAGGGAGGCTCCTGACAGGTGCCCTTTGTCAGAC
CCTACCACAGCCTGGATAGGCAGCCACATTGGTCCTCGCCCTTGCTCGGCACTCCGTGGT
GGTCCTGCCCTTCTCCCTGCATGCCTGTGGGTCTGCTCTGGTGTGTGAAGGTCGGTGGGT
TAACTGTGTGCCTACTGAACCTGGCAAATAAACATCACCCTGCAAAGCCTCTGGCCACCC

6242 GGAGAGGCTGGGAGCAGGTTCACAAGTAGTGGCTGGGAGTAGTAGTGAACAGTGCCCTGT
GGATTTCTTGGGCTGAGGGTGAAGATCATCCTCACCACAGTGTATTCCTCAATGGTGGTG
GTGGTGGGGGTCCTCTGAACTCTAGAAATCCATGTGAGTAGTGGGTCTTGGGCTGCATTT
GGACCAAGGAATACTCCCTGGGCTGAGAGCTCAAGTAAGGGCTGCTGTTTTTGACTCCTG
TTGACCGAGGAGCCTTACTCTTGATTTAGGCATAGAGCTGGAATCTACCTGGGCCAGCCA
[G,C]
CGCAAGGACAGACCCTGCTCATAGCCAAAGATAGCTTCCCTGAGCTAGGGAGAGGGTGTA
GGGTGAGCAATGCACAAAGATTCTATGCTGCTCTGTGTTGATTCCTTCTTTCTGTGAACA
CCTGTGCTTTCCACCTATGCCCCAAATGAAATCTCACTCTGGGTCTATTTCAGCTGGAGC
AGATCAGCTTTATATTATGGGACTATGCACAGGGTTTCTTCTGGGTAGAGGGAGTAACAC
TGCCACAGATACTAAGCCTAAAAACCCAAAAGTTGACTTACTCCAGCCCAGGTGGGCCTG

FIGURE 3E

7264 CTATTCCCTTGCGGCTGCGGTTTTCTCTGCCTTGGCCCAGCCTGCCTCGCGCCAGCTCTG
GCATGGGACCACAATGCGCTGCCTTGCCCTGGAAAAGGGTCCAGCTGGCAGCCTCGCTGC
TCCCCGCCTTGATATAATGCTGCGCTCTCAAGTGGCAGGTCGAGTCTCCCCAGAGGACGC
CTGAGAGCGACCGCGCTCCGCCCAGGATTCTCTACGGCCTCGGGGCCGCTAAGCCCCGCC
CATAGTTCCGCCCATCCGAGAATTTGTCCAATCCAGGCGAAGTATTCACGCTCCGCCCAA
[G,A]
GTTTTGTGTTGTCACTTCCGGCCCGCTCCAGGAAGTCGTGCTGCGGAGCCAAATTTGAAG
CAAGCGGAGGCGCGGGGGCGCGTCTACGAAGCCGGACCTGTAGCAGTTTCTTTGGCTGCC
TGGGCCCCTTGAGTCCAGCCATCATGCCTATCCGTGCTCTGTGCACTATCTGCTCCGACT
TCTTCGATCACTCCCGCGACGTGGCCGCCATCCACTGCGGCCACACCTTCCACTTGCAGT
GGTGAGTGACTGCAGTGTTGGGGCCCGGTGTTTGCCCG

FIGURE 3F